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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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             175
172.6
165.2
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12849.734 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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                      BH487741 BOGWB48TR
AL080416 Arabidops
BM270448 Sakla03.
BH477964 BOHKJ17TR
BH462017 BOHNZ43TR
AZ686821 ENTL174TR
AL514901 AL514901
AL106171 DYCOSOPhil
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B97951 F22C23TFB I
BH530370 B0GD070TF
BF291837 WHE2204_E
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BH530380 B0GD070TR
BH462012 BOHNZ43TF
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 BE420736 HWM002.A0
AL060732 Drosophil
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18 67.8 3.2 330 9 AL5J3817 19 67.8 3.2 410 9 AL5J3713 20 67.6 3.2 410 9 AL5J3713 21 67.6 3.2 590 9 AL5J3713 21 67.6 3.2 590 9 AL5J3721 22 67.4 3.1 613 12 AQ92Z590 23 67.2 3.1 613 12 AQ92Z590 24 65.8 3.1 987 12 CNSO14PQ 25 65.8 3.1 401 9 AL5J5711 26 65.8 3.1 401 9 AL5J5711 27 65.8 3.1 401 9 AL5J5711 28 65.6 3.1 429 9 AL5J5711 29 65.6 3.1 529 9 AL5J5711 29 65.6 3.1 529 9 AL5J3713 30 65.6 3.1 523 9 AL5J3713 31 65.4 3.1 421 19 AL5J3713 32 65.4 3.1 421 19 AL5J3713 33 65.4 3.1 421 10 BM270739 34 65.2 3.0 777 12 CNSO25WB 35 65.2 3.0 988 12 CNSO27ZR 36 65.6 3.0 230 9 AL5J8612 37 66.6 3.0 230 9 AL5J8612 38 64.6 3.0 230 9 AL5J8712 39 64.2 3.0 618 10 BM270738 40 64.2 3.0 65.1 10 BM270739 41 64.2 3.0 951 12 CNSO0AQX 42 64.3 3.0 954 12 CNSO0AQX 43 64.4 3.0 954 12 BM270732 44 63.8 3.0 979 9 AL5J772 45 64.4 3.0 954 12 BM270739 46 57.2 CNSO0AQX 47 61.2 3.0 51 10 BM270739 48 3.0 453 10 BM270739 49 AL5J3713 BM270739 40 64.2 3.0 618 10 BM270739 41 64.2 3.0 551 12 CNSO0AQX 42 64.3 3.0 954 12 BM270752 43 65.4 3.0 954 12 BM270752 44 63.8 3.0 954 12 BM270752 45 65.4 3.0 954 12 BM270752 46 65.4 3.0 954 12 BM270752 47 67 12 CNSO0AQX 48 63.8 3.0 954 12 BM270752 49 AL5J3713 BM270752	\L51397		3.0	w	4 51	a
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ALIGNMENTS

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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
B10183
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Other_GSSs: F19N12-T7
Contact: Ecker J.
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                                                                                                                                                               High quality sequence start: 87
High quality sequence stop: 806
Location/Qualifiers
                                                                                                                                                                                                                                                                     Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B10183.1 GI:2091302
                                                                                                                                                                                                                                 Class: BAC ends
                                                                                                                                                                                                                                                      Seq primer: Sp6
                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis Thaliana Genome Center University of Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                          of Biology, University of Pennsylvania, Philadelphia,
                                                      /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="F19N12"
/sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
                                      /clone_lib="IGF"
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879 tcgatgatgagtcatctgagcaacgttcagagatatattcacagtattccgacttcgatt 938
                                                                                                                                                579 cacgatccgatgtgaccttcgccggacatgtctccaacagccggagtttgaatttcgaat 638
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Location/Qualifiers
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Seq primer: M13-21
Class: BAC ends
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Tel: 301 838 0200
Fax: 301 838 0208
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Steve Rounsley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 192)
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golder, Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter
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F22C23TFB IGF Arabidopsis thaliana genomic clone F22C23, DNA
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3 c 50 g 48 t
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/note="Vector: BeloBACII; Site_1: ECORI; Site_2: ECORI;
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                                                                                                                                                                                                                                                                                         261
                                                                                                                                                                                                                                                                                                                                                          201 tototocogttottgttoaatcacotototggagcaaaacaaatcggagtototgctgctt 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 AAGTTTCGTGTCACAAGATGAAGGAGATGGCGTCGAGGATTTCAAAGCGCAAGGCTGAGC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 AACGAACTTCCATTTTCGAATTTGAAA--TCTGAATTCGAATCTAAAACTTTCTTCGGAG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 aacgaacttccattttcaaaattcgaatttctaatttctagtttcaagctttcgtacg-- 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                           cgacgccgttcgccgggaagaagctccggtcgacgcgattacgccggaagagagacacaga 200
                                                                                                        aacctggttataatgt---gaaggagacgattggtgattcgaaatttcgaaggattacga 431
                                                                                                                                                                                                                                                                                           ctgtcgattcctgctccgatttgct-----agctgatgacaacgtttcctgtggttcga
                                                                                                                                                                                                                                                                                                                                                                                                                     CGACGCCGTTCCCCGGGAAGAAGCTTCGATCGATTCCATCTCGCCGGAAGAGAGCTCAGA
GATCATACTCTAAGCTAC-CAAGGAGAAGATCATAGATGAGACTGAAGCA 818
                                                                                    GACCTGGTAAAGATGTAAAGAAGGAGACGATCGCTGATCCG - AAGTTCGGAGGATCACTA
                                                                                                                                                                 GCAGAGTCGAGAAGAGCT-----TCGGGAAGAATCGAATTGAAGAGGAAGAAGTTTCTC
                                                                                                                                                                                                        gcagagtcgagaagagctcgaatccgaagaagactctaattgaagaggtagaagtttcta 374
                                                                                                                                                                                                                                                    CCGTTGATTCCTGCTCCAATTTGCTCTCTGCAGTCGACGACAACGTTTCATGCGGTTCTA
                                     ggtcttactctaagctacacaaggagaaggaggagatgagatcgaagta 481
                                                                                                                                                                                                                                                                                                                                      TATCTCCAGTTTCTATCCAGCCACCTCTCT-GCCAAAGGAAGTAGGAGTATCCGCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOGDQ70TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 818)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOGDQ70TF BOGD Brassica oleracea genomic clone BOGDQ70, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH530370.1 GI:17746915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a    186 c    168 g    200 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Brassica oleracea"
/strain="TO1000bH3"
/db_xref="taxon:3712"
/clone="BOGDQ70"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="BOGD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 188.8; Db 14,
Pred. No. 2.3e-16;
Pred. No. 2.3e-16;
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RESULT
BF291837
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                 Matches
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1370 aaaagggaaaggactctaatactagtcgggattgcgagtcttactctggccaccagaatt 1429
                                                                                                                             1430 gaagaaatcaaccttacaacagcatccggaaaaggaacttcaccattcagaacctaaga 1489
                                                                                                    64
                                                                                                                                                                                                4 AAAGGCTCTAGGAATGTGCAGTTGCTGGGCATTGCCTGCATCACCCTAGCCACCCGCATT 63
                                                                                                 GAAGAGAACCAGCCATACAATAGCATCATGCAGAAGTCTTTCATGGTAGGGATCAACCTT 123
                                                                                                                                                                                                                                                                                                 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The structure and function of the expressed portion of the wheat genomes - Anther cDNA library from Aegilops speltoides Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF291837
531 bp mRNA linear EST 17-NOV-200 WHE2204_E10_J202S Aegilops speltoides anther cDNA library Aegilops speltoides cDNA clone WHE2204_E10_J20, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Close,T.J., Fenton,R.D, Han,P.S., Hsia,C.C., Kang,Y., Kianian,P., Lazo,G.R., Miller,R., Otto,C., Rausch,C.J., Seaton,C.L., Simons,K., Tong,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aegilops speltoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticeae; Aegilops.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
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                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-Tvector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in a growth
Chamber at the University of California, Davis (Akhunov).
Premeiotic anthers were harvested, total RNA and poly(A)
RNA were prepared, from each tissue and then pooled, a
cDNA library was made, and the CONA clones were in vivo
excised to give pBluescript phagemids in the Ty Close lab
(Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons,
Zhang) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="whE2204_E10_J20"
/clone_lib="Aegilops speltoides anther
/tissue_type="Anther"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Premeiotic anthers"
/lab_host="E. coli SOLR"
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/cultivar="F2 from 2-12-4-8-1-1-1-(1) x PI36909-12-811-(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                      8.2%;
61.5%;
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                               Score 175; DB 10;
Pred. No. 1.8e-14;
0; Mismatches 175;
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AUTHORS
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Best Local :
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                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAC End Sequences at ATGC Unpublished (1997) Other_GSSs: F1C14-Sp6
                                                                                                                                                                                                                                                                                                                                                                  Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                  Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                               Email: jecker@atgenome.bio.upenn
                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 215-898-9384
Fax: 215-898-8780
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Ecker J.
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F1C14-T7 IGF Arabidopsis thaliana
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                                                                                                                                                             308
                                                                                                                                                                                                                                                                                                                                  quality sequence start: 37 quality sequence stop: 889
                                                             Conservative
                                                                                                                                                                /sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2:
Produced by Thomas Altmann"
                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
/strain="Columbia"
                                                                                                                                                                                                                        /clone_lib="IGF"
                                                                                                                                                                                                                                       /clone-"F1C14"
                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                           Score 172.6; DE Pred. No. 3e-14; D; Mismatches
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                                                                                           DB 12;
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                                                                                                                                                         2 others
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                                           AACTTCTTATGGTAAAAACCTCTATTACTATATATTTTCTGTTCCGAGACACATGCACAC 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: in Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rossidae; eurosids I; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
BH530380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Other_GSSs: BOGDQ70TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 803)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
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GSS.
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BOGDQ70TR BOGD
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                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                           /Glone_lib="BGGD"
/Glone_lib="BGGD"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
128 c 181 g 253 t
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                       /clone="BOGDQ70"
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Pred. No. 3.3e-13;
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1761 aggtcc 1766
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                                                                                                                                                                                                                                                                                              Match 7.1%; Score 152.4; DB 12; Local Similarity 88.7%; Pred. No. 2e-11;
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                                                      GGCTTGTAGTTCTCGCCTGCAGTGAACACAACAAAATCTCAGCATACCAACGAGTCATAA
                                                                                                                                                                                                                                                                               165;
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Brassica viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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BOHNZ43TF BOHN Brassica
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Other_GSSs: BOHNZ43TR
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
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Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea.
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is from a doubled haploid
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
a 70 c 116 g 153 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Brassica oleracea"
/strain="TO1000H3"
/db_xref="taxon:3712"
/clone="BOHNZ43"
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                                                                                                                                                                                                                        ttgagatagtcggatgcgtctctgatctcgcttgctctgagaaaattctcggaaagaggttt 869
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                                                                                                                                                                                                                                                                                                                                                           TCGGAAGCGTAACCGGAGGAGGAGGAGGAGGCGATTACGAAGAAACCGAAATCTCCAAAC 343
                   agaaatcttcctctgattctcctatttcacattctcgctctctgtacctccagttcaagg
                                                    -----TCGGATTACACTTCTTCAGTTTTCTCCGACTCTGGCAGCGAGTTCTCTG
                                                                                       acttcgattactcggattacactccgtccatcttcttcgactctggcagcgaattctctg 989
                                                                                                                                                                                                        TTGAGACAGTCGGATTCGTCTCCGATCTCGCTTGCGCGGAGACGTTCTCCGACGAAGAGG 433
                                                                                                                                                                                                                                                                                                                                                                                          tcgggagcgttaccggaggagct-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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ilarity 67.9%;
Conservative
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/clone_lib="BOGW"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
a 168 c 196 g 175 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOGWB48"
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1. .727
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Pred. No. 8.1e-11;
0; Mismatches 66
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                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           CAGTTCTGTAGATCCACGATTCCCAACGATTTTGGATCTTCTTGCGAGGAAGAAATTCAC 120
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Phaseoleae,

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                 498 bp mRNA l sakl3a03.yl Gm-c1075 Glycine max cDNA clone Gm-c1075-2717 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                 soybean
                                                                                                                  EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Salanoubat,M., Choisne,N., Artiguenave,F., Brottier,P., Wincker,P.,
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/clone="F1C14"
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/strain-"Columbia"
/db_xref-"taxon:3702"
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Pred. No. 1.3e-06;
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                1812 tggactggttgcttgggcagtaagca
                                                                                        1752 gagtcataaaggtccatgttagaacaacagataacgagttgcctgaatgcgttaagagtc 1811
                                                                                                                                                                                1692
                                                                                                                                                                                                                                  1632 aatccttggctgttacctcactatccgaccaaactccaactctgttttttggccctcaactg 1691
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This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Shoemaker,R., Keim,P., Hiller,L., Kucaba,T., Martin,J., I., Bolla,B., Marra,M., Hiller,L., Kucaba,T., Martin,J., I., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., I., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., N., R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Public Soybean EST Project
Washington University School of Medicine
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www.resgen.com
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
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                                                                                                                                                       The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an xhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by xhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DHIOB host cells. Tissue culture and library construction were performed by Francoise Thibaud-Nissen and Anu Khana (Lila Vodkin lab, University of Illinois)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhOI; The cDNA library was constructed from mRNA isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from differentiating somatic embryos cultered on MSM6AC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="differentiating somatic embryos cultered
MSM6AC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Glycine max"
/db_xref="taxon:3847"
/clone="SovEBEAN CLONE ID: Gm-c1075-2717"
/clone_lib="Gm-c1075"
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96.4; DB 10;
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Beck,C.,
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                                                                                                                                                                                                                                                                                               1829 cagtaagcaatcaaaaagaacaaaaacccta--aaaccaggacacagtatact-ccgata 1885
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                                                                                    2058 ttcattagactctcatattcttaaaaagaatatt 2091
 314
                                                                                                                                                                                                         139 CGAACTCACAGGTTATTATTACCATTTA-TTAAACAAATAGTATATAATTGGTATAAACT 197
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                                                                GCATACTAATACCAATTATTTGTGTCGC-CACCAAAATTTATTGCTTATTTTTCCCAA 313
                                                                                                                                                                                                                                                                              CAGTAAGCAATCAACAACAACAATACCCCCCCAAACCAGAACACAGTATACTCCCCATA 138
 TACACTACACTCCCATTTTATTAAAAATCATTTT 347
                                                                                                                                                     -----ctctacagatttatatacttaatcgagctggacttaattagctcttagtat 1997
                                                                                                                                       AAGCAATGCCTCTACAGATTTATATACTTGATC - - - TCTGGACTTTTTAGCTGTTGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOHKJ17TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Chris Town
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is from a doubled haploid
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ilarity 67.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="Taxon:3712"
/clone="BOHKJ17"
/clone_lib="BOHKJ1"
/clone_lib="BOHKJ1"
/clone_lib="BOHK"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/genomic DNA inserted into pHOS1 using BstXI linkers"
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                                                                                                                                                                                                                                                        CGATCCTGAAGATAGCTCTGATCTCTCC
                                                                                                                                                                                                                                                                                                                         ATTCAAAGCGTAAGGCTGGGGGGGACGCCGTTCGCCGCGAAGAACCTTCCGTCGATGAGTT 493
                                                                                                                                                                                                                                                                                                                                                                                           AATTCGAATTTGAAATTTTCATCGGAGAAGTTTCGTCGATGAAGGTGATCGCGTCGAGGA 433
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Other_GSSs: BOHNZ43TF
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Eukaryota; Viridi
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BOHNZ43TR BOHN Brassica oleracea genomic clone
                                                                                  genomic, DNA sequence.
AZ686821
AZ686821.1 GI:11823967
GSS.
                                                                                                                                    791 bp ENTLI74TR Entamoeba histolytica genomic, DNA security
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DNA is from a doubled haploid
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Tel: 301-838-3523
Fax: 301-838-0208
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              Eukaryota; Entamoebidae; 1 (bases 1 to 791)
                                                Entamoeba histolytica
Entamoeba histolytica
Loftus, B., Van Aken, S. and Fraser, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="BOHN"
/clone_lib="BOHN"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
1 156 c 116 g 143 t
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/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHNZ43"
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BOHNZ43, DNA
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1844 aagaacaaaaaccctaaaaccaggacacagtatactccgataccaacacacaggttatca 1903
                                                                                                                                                                                                                                                                                                                                                                                                                       1904 ttactatttacaaaaacaaacacacaaggtaagtaataagaactcctctacagatttatata 1963
                                                                                                                                                                          2144 a 2144
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                            prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: shotgun
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Seq primer: M13-Reverse
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/clone="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University press, 1999)."

78 c 45 g 393 t
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/strain="HM1:IMSS"
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Pred. No. 1.5;
                                                            mRNA
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                                        RNA linear EST 13-FEB-2001 CDNA clone CL0BB012ZH12 3
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                                                                                    Drosophila melanogaster genome survey sequence SP6 end of BAC BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Contact: Genoscope
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/note="Vector: pcWYSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcWYSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMYSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliangelifetech.com URL:
http://fulllength.invitrogen.com"
23 a 52 c 34 g 333 t 126 others
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/db_xref="taxon:9606"
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fruit fly.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 132699)
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Gonzalez, A., Hansen, N.F., Huizar, L., Kremenetskaia, I., Lenz, C.,
Li, J., Liu, S., Luros, S., Rowley, D., Schwarts, J., Toriumi, M.,
Li, J., Liu, S., Luros, S., Rowley, D., Schwarts, J., Toriumi, M.,
Theological M. and Unpublished Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome Vysotskaia, V., Yu, G., Davis, R.W., Federspiel, N.A., Theologis, A. and

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SUMMARIES

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Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,

Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,

Liu, S., Mukharsky, N., Mguyen, M., Palm, C., Pham, P., Sakano, H.,

Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,

Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (07-MAY-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-FEB-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 3 (bases 1 to 132699)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
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Join(6881 7029,7140 7296,7392 7876,7961 8180)
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EST emb|F14394.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAF79217.1"
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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                                                                                                                                                                                                                 GGTAGAAGTTTCTAAACCTGGTTATAATGTGAAGGAGACGATTGGTGATTCGAAATTTCG
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                                                                                                          aaggattacgaggtcttactctaagctacacaaggaggagaaggaggagatgagatcgaagt 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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similar to EST gb|N96048.1"
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/evidence=not_experimental
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo 72 c 1014 g 2655 t
                                                                                                                                                                             Location/Qualifiers
                                          3.7%;
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AX344555
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                                                                                                                                                                                                                                                                   /note="chemically treated genomic DNA (Homo sapiens) -Cristially treated genomic DNA (Homo sapiens) -Cristian length of seq 1: 3.673778 <223>-split as follows: -seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 01 0.000.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.749.980-seq 08 2.100.001 2.449.980-seq 07 1.800.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.749.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.63.778 <223>-cristian length of seq 2: 3.673778 <223>-split as follows: -seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.749.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 3.349.980-seq 23 2.700.001 3.049.980-seq 25 3.300.001 3.049.980-seq 26 3.600.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001
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/db_xref="taxon:32630"
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No. 5.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sparrow,D.B., Miska,E.A., Langley,E., Reynaud-Deonauth,S. Kotecha,S., Towers,N., Spohr,G., Kouzarides,T. and Mohun, MEF-2 function is modified by a novel co-repressor, MITR EMBO J. 18 (18), 5085-5098 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEF-2 co-repressor; MITR gene. African clawed frog. Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                 1489
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        /db_xref="SpTrembl:Q9YGY4"
//db_xref="SpTrembl:Q9YGY4"
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KEQKMEQQRKEGEAERHRQEQQLCHPRSKDRVKERAVASTEVKOKLQEFILSKSATKE
PLTNCTSHSMCRHPKLMYTAAHHTSLDQSSPEPSGTSPTYKCPPPGNQDDFPLRKTAS
EPNLKVRSRLKGKVVEERSSPLLRKDSIVSSSYKKRIEPSAESSYSSSSSEVSGPSSP
PLTNCTSHSMCRHPKLMYTAAHHTSLDQSSPEPSGTSKTKCPPGRQDDFPLRKTAS
EPNLKVRSRLKGKVVEERSSPLLRKDSIVKSSYKKRIEPSALSULNLXTSPSLFNITLGLHA
TATOLNTSSSLKEQQKYDPQAPRQGVSMAGQYAGGIPTSSNHVSLEGKANSHQAILQH
LLKEQMRQOKILASGGTPVLHQSPLAAKDRYSPAGRVAKLPRHRPLGSAPLPQ
STLAQLVIQQOHOLEKGKOYQQQIHMNKILSKSIEQLRQPEGHLEEAEEDLHGDNL
MQEKSSSIDNTRSYSSTDLRTGFFGSVVKEEPPDSENEIKTHLQSEQKSVFAQQVT"
89 a 866 c 806 g 1274 t
                                                                                                                                                                                                                                                                    /product="MITR protein"
/protein_id="CAB10167.1"
/db_xref="GI:3955063"
                                                                                                                                                                                                                                                                                                                                                    /gene="MITR"
                                                                                                                                                                                                                                                                                                                                     /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                             /gene="MITR"
121. .1818
                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:8355"
121. .1818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Xenopus laevis"
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NW7 1AA, United
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Local

3.3%; Similarity 78.0%;

Conservative

Score 70.6; DB Pred. No. 3e-06; 0; Mismatches

24;

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Length 4435;

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               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTTTTTTTTTTTTTGCCTTATGTTATAATATTATTCTTTTCACAAATAAAAAGTTTTCT 4363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-JAN-2002) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC107226 149791 bp DNA linear HTG 17-JAN-20 Oryza sativa chromosome 3 clone OSJNBa0081P02, *** SEQUENCING IN PROGRESS ***, 10 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Saski,C., Henry,D., Oates,R. and Simmons,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T., Saski,C., Henry,D., Oates,R. and Simmons,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice Genomic Sequence
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This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                           the accession number will be preserved.

1 1837: contig of 1837 bp in length
gap of unknown length
1838 21394: contig of 19557 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by the finished sequence as soon as it is available and
                                                                                40949 a
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                                                                             /chromosome="3"
/clone="OSJNBa0081P02"
33193 c 33129 g 42
                                                                                                                                                             1. .149791
                                                                                                                              /organism="Oryza sativa"
/db_xref="taxon:4530"
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contig of 7296 bp in length
gap of unknown length
contig of 2153 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                           gap of unknown length contig of 25125 bp in length
Score 68.6; DB 2;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                             unknown length of 15716 bp in length
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57534 CAGTGGTAGCCCTTGCCTTGCCACAAACAATGAGTCATGATTATGGCTTATGG 57475
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                                                                                                                                                                                                                                                                                                                                                                                                                      prim_transcript 1163.
                                         prim_transcript
                                                                                                                                                                     prim_transcript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (sites)
Paure,M., Franke,J., Hall,A.L., Podgorski,G.J. and Kessin,R.H.
The cyclic nucleotide phosphodiesterase gene of Dictyostelium discoideum contains three promoters specific for growth, aggregation, and late development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Draft entry and computer-readable sequence (1989) In press] kindly provided by R.H.Kessin, 23-MAR-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The cyclic nucleotide phosphodiesterase gene of Dictyosteliur discoideum utilizes alternate promoters and splicing for the synthesis of multiple mRNAs MOL. Cell. Biol. 9 (9), 3938-3950 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Mycetozoa; Dictyostelium. 1 (bases 1 to 6372) Podgorski, G.J., Franke, J., Faure, M. and Kessin, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyclic nucleotide phosphodiesterase. D.discoideum (strain NC4; cell line AX3-K) DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyoselium discoideum cyclic nucleotide phosphodiesterase gene,
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1780. .4077
2173. .2180
2267. .2376
                                                                                                                                                                     join(2267
2267. .600
                                                                                                                                                                                                                                                                                                                                           join(1163.
1163. .177
                                              join(3689, 3689, 606
                                                                                               3663.
                                                                                                                    /note-"vegetative promoter" 2377. .4077
3689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Dictyostelium discoideum"
/db_xref="taxon:44689"
                    /note="late promoter"
                                                                                                                                                                                                                      /number≖
                                                                                                                                                                                                                                                                                                                                                                     /note="aggregation promoter"
join(1163. .1779,4078. .4146,4297. .>6060)
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Best Local Similarity 51.18;
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Sequence 9 from Patent WO0200932.
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SSFLITKKGSNLFIALDAGTVØQGVRRLTTFKYENTILFNITYBEWAVLFEQRTSWFLK
NHYMSYFIGHSHLDHVGGLILVSPEDYLAKIMIDDVQPFINNGIMGLIKLGFKFDYDFT
SSSILQKKTIMGLESTINSISTNLFNNQVWPNLFSFGRYQYFSLASGIEYPFTELYPF
VATTMSLVANEFPFSVKVKPFELCHDNLISTSFLFTDSISGEQIAFFSDTGVPSSVAC
DWEGKIYAVWKQIKIDKLKAIYIETSFPNNTDSSAFFGHLRPBJVMKLMDQLLVQSIO
             /organism="synthetic construct"
/db_xref="taxon:32630"
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/protein_id="AAA63168.1"
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/translation="MALNKKLISLLLLIFIILNIVNSHQQEDCDDDDEDIGISAERSE
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/codon_start=1
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/EC_number="3.1.4.17"
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Pred. No. 1.8e-05;
0; Mismatches 151; Indels
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Best Local Similarity 51.3%;
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Submitted (02-0CT-2000) Institut fuer Biochemie I, Medizinische Fakultaet, Universitaet zu Koeln, Joseph-Stelzmann-St. 52, Colog 50931, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 7736)

Rivero,F., Dislich,H., Glockner,G. and Noegel,A.A.

The Dictyostelium discoideum family of Rho-related processes and color and colo
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Dictyostelium discoideum
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Rivero, F., Dislich, H. and Noegel, A.A.
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AF310889
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Pred. No. 2.6e-05;
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/product="unknown"

join(856. .1007,1160. .4670)
/note="5' region identified manually, therefore unsure;
similarity to mouse SH3-domain containing adaptor prote
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/note="corresponds to EST clones SSB614, SSG550, SSJ204
/notes="corresponds to EST clones SSB614, SSG550, SSJ204
and SSK792 from the Japanese cDNA sequencing project; cDNA
(partial) already described in L11594."
/product="RacD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQQQQSVDKPIERPSKPPPPKRTAAMNSSINNINEPPPPSNKPPPPPKSLKPLSTSD
GYEPPSPPSSSSTTPITTSGEDTLQKSPTLQRKVAPPPQQQNEQDLPSSIVGKPPPLK
PTPKPRAIQTNSESTAPAPTPSHEVNFKANLKPAKPSSPPIGNSQEIPTDTSSPPNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KITSLFKKPLKKITAISALTGSHSSNESSSGGDKNNSGSKTKAKVVYDFESKEPNELN
LKKGDIIVVLAKDSSGWWQGINQSTQATGWFSNTFVEEIKEEKLPPPPSSSENKQPLK
IVKSPPPKSSSSSQPQTVEAKLQSLSDTPKLETARKAGAAKGRKPPSRVRASYLLSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEEEISKPISQVSRLGINISLGSMDELKNKLAYRKTATYTSADIEEAHNNNNASNEES
NSSSSSSSNINSSGGFVAVKPSGAVNTQQRQPGKVLLNNRQSTILSGVPPAIQSIP
SSNTNTTTTTNTTPAVQPLIQLKPKQTNTEINTSGNSIPATTSKESQSTKEESSSGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="aag45120.1"
/db_xref="GI:12007301"
/db_xref="GI:007301"
/translat.ton="merwhOsunLvyvTenidanvTkQDIHABITSSSTGLGVKGFGL
/translat.ton="merwhOsunLvyVTenidanvTkQDIHABITSSSTGLGVKGFGL
NCEVCIFIKGSKWAIKDDTVQVQMDKQQTGVKWSHLLSEITESNAKAVVLFEYEATSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FNCLEMYDNKPVNLVLMDTAGQEDYDNLRPLSYPQTDVFIICYSVVKRDSLDNIKYKW
LPEINQTNQGTPIILVGTKTDLREDKKTLSQLQESKQEPVSRDEGVALAKEIGAVQFF
ECSALTGNGVNDIFAAAIKAAFNKPAVTSPTSKSSGKSSPSSTSSKPSKTTTTTTTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Rho-GTPase;
of Rho proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STQFLNIIQELVNCSSVSCDMVSYLSQKSETSDEILVGHLLKSSGLIKQPDDVLDFFY
QINSIQLNSKQVSVLAATLANDGVCPFSQDLKLAPKNIISKTIDLIRICNSTPITSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="AX4"
/db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKAEREKLKQSFYSHVVSSQKELSMYDNNEDGGEHLSDDDQPSTPPSISRSGGSFTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EELSLIPHQVIDIISKDDSGWWEGSKQQMNGVFPSNFVQEFPTDYQPPEDEDASAEAT
                            ALSLVFKLYSRVLK"
                                                               EYKQILSFTKNSYVVAQVIRGLIKCVTSFWTSLTPNQKNDMKSNIWLYIESVQPLEQF
                                                                                                                                                                                                                                                                     /product="unknown"
join(7278. .7533,7645. .>7736)
                                                                                                                                                                                                                                                                                                                                                                                                                             SSSSPPAASTAKPAGEKKLSWGLFRKKDKDEKKPAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id-"AAG45121.1"
/db_xref-"GI:12007302"
/translation-"MATGIKKTYKVYYVGDGAVGKTSLLILYTTKAFPKDYVPTYFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"RacD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="racD"
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(C-terminal part)"
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                                                                                                                    /protein_id="AAG45122.1"
/db_xref="GI:12007303"
                                                                                                                                                                                                                                                                                                                                    )oin(<7278.
                                                                                                                                                                                                                                                                                                                                                          /gene="racD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="racD
                                                                                                                                                                                /product="unknown
                                                                                                                                                                                                             /evidence-not_experimental
                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                           translation="MSIQSEQDFFKFEELCKDFYLKPEETIKIDDILHQYFLNPNFLI"
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4 from Patent W00200932. Ax344553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosis of known genetic parameters within the Patent; WO 0200932-A 4 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olek, A., Piepenbrock, C. and Berlin, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic construct
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                                                      Sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 06 1.500.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 07 1.800.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length of seq 2: 3.673778 <223>-split as follows.-seq 14 0.000.001 1.549.980-seq 18 1.200.001 1.549.980-seq 17 00.349.980-seq 18 1.200.001 3.649.980-seq 18 0.000.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.0
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/note="chom:"
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                             g 172166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149;
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3.1%;

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DB

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Length 349980;

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DEFINITION
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TITLE
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Best Local :
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1917 aaacaaacacaaggtaagtaataagaactcctctacagatttatatacttaatcgagctg
                                                                                                                                        Local Similarity hes 149; Conserv
                                            CAAATACACAAACAACGATTATACTAAACCCAACCTAAATTTAATAATTCCGAAACAAAA 49140
                                                                       ctaaaaccaggacacagtatactccgataccacacacaggttatcattactatttacaa 1916
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Sequence 5 from Patent WO0200932.
AX344554
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                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                  /note=*chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 1.249.980-seq 03 600.001 2.449.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 06 2.100.001 2.449.980-seq 07 1.800.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.749.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length of seq 2: 3.673778 <223>-split as follows.-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 0.001 3.673.778 <223>-Original length of seq 2: 3.673778 <223>-split as follows.-seq 16 0.300.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.449.980-seq 21 2.100.001 3.000.980-seq 22 2.400.001 3.349.980-seq 23 2.700.001 3.000.980-seq 26 3.600.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778
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Pred. No. 6.3e-05;
0; Mismatches 139;
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AX344574/c
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caccatttgtgt---cgctcatacacatttatttcttattttccctaattcattagactc 2069
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AX344574
AX344574.1
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artificial sequence.
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/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                       Score 65; DB Pred. No. 8.7e 0; Mismatches
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8.7e-05;
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Best Local Similarity 54.5%;
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                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1990)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guartin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Vi, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 545)

Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
Genes, compositions, kits, and methods for identification,
                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                 fruit fly.
                                                                                                                                                                                                               AY069454.1 GI:17862243
                                                                                                                                                                                                                                            AY069454 1090 bp mRNA linear Drosophila melanogaster LD17744 full length cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assessment, prevention, and therapy of cervical cancer Patent: WO 0142467-A 1400 14-JUN-2001; Millennium Predictive Medicine, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1400 from Patent WO0142467
      Direct Submission
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1. .545
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                           aaaaaaaaaaaaaaa 2144
                                                                                                                                                                                                                                                                                                                               Sequence 4041 from Patent WO0142467 AX188346
AX188346.1
                                                                             AX188346
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Sequence submitted by:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation-"MSLGNADPWHLKNTIVKQGISGSANNSESFEDNETPLPSGNESN/translation-"MSLGNADPWHLKNTIVKQGISGSANNSESFEDNETPLPSGNESN/VKDCKDGKIEPLPSGNESN
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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Best Local Similarity 75.2%;
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                                                                 AAAACAAATTAAAACCCCAACCGCACACCTACTTCCTAAATTCGCTATAATACCTAAAAC
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artificial sequence.
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1 (bases 1 to 1298)

Schlegel,R., Deeds,J., Berger,A. and Zhao,X.

Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer Patent: WO 0142467-A 4041 14 -UNI-2001;

Millennium Predictive Medicine, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 96 from Patent
AX345025
AX345025.1 GI:18492911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epigenomics AG (DE)
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/db_xref="taxon:9606"
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1. 1298
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/note="chemically treated genomic DNA (Homo sapiens)"
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Search completed: July 25, 2002, 09:08:40 Job time: 11330 sec

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1: /cgn2_6/ptodata/2/.

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Query Match Best Local Simi Matches 80;	US-08-446-855A-1 US-08-446-855A-1 US-08-446-855A-1 Sequence 1, Application US/08446855 Sequence 1, Application US/08446855 APPLICANT: Stewart, Thomas S APPLICANT: Flores, Maria V APPLICANT: Flores, Maria V APPLICANT: Flores, Maria V APPLICANT: O'Sullivan, William TITLE OF INVENTION: Nuclectide TITLE OF INVENTION: Nuclectide TITLE OF INVENTION: Sudderhye STATE: Virginia COUNTRY: USA INTERET: 1100 ND. 5849573th Gl CITY: Arlington STATE: Virginia COUNTRY: USA INTERET: 1100 NG. 5849573th Gl CITY: ARLINGTON STATE: Virginia COUNTRY: USA INTERET: 1100 NG. 5849573th Gl CITY: ARLINGTON STATE: Virginia COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: F		28 28 29 30 31 31 31 31 31 31 31 31 31 31 31 31 31
larity Conserva	Application US/0844685 5849573 FORMATION: TIT: Stewart, Thomas S TIT: Stewart, Thomas S TIT: Stewart, Thomas S TIT: Stewart, Thomas S TIVENTION: William INVENTION: William INVENTION: William INVENTION: William INVENTION: William SEE: Nixon & Vanderhye IIO NO. 5849573th G Arlington Virginia V: USA 2201-4714 READABLE FORM: TYPE: Floppy disk TYPE: Patentin Release # APPLICATION NUMBER: US/08/44 APPLICATION NUMBER: US/08/44 DATE: 06-Jul-1995 INTION NUMBER: 29.009 ENCE/DOCKET NUMBER: 47- MITCHATON HOMBER: 47- MINICATION INFORMATION: MITCHATON NUMBER: 47- MINICATION INFORMATION: ONE FOR SED ID NO: 1: CHARACTERISTICS: H: 8920 base pairs Ducleic acid ETYPE: genomic ETYPE: genomic		22 24 5 5 5 5 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6
2.8%; 70.8%; tive	US/08446855 Thomas S Maria V An, William Nucleotide phosphate s SS: SS: SY disk DY disk DY disk DY disk SY Holder Holder PC-DOS/MS-I ARRION: BECAUTION:		2409 4 221409 4 22144 1 3238 4 3238 4 4588 1 2280 2 1212 2 1212 2 1212 2 1212 2 1212 2 1212 2 1212 2 1213 3 1483 3 1483 3
Score 60.2; DB 2 Pred. No. 9.6e-06 0; Mismatches 3	855A am J am J de sequence encod e synthetase II ye PC Glebe Road, 8th Glebe Road, 8th 446,855A	ALIGNMENTS	US-09-293-322C-8 US-07-263-622E-6 US-07-263-622E-6 US-08-123-934A-5 PCT-US94-10080-5 US-08-452-550-7 US-08-68-717-717-1 US-08-613-150-1 US-08-688-988-44 US-09-292-770-18 US-08-688-123-41 US-08-688-123-41 US-08-688-123-41 US-08-582-298-20 US-08-582-298-20 US-08-582-298-20 US-09-262-749-1 US-08-860-339-17
; Length 892 ; 3; Indels	oding carbamoyl		Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
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; ORGANISM: Plasmodium falciparum
US-09-150-741-1
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SEQ ID NO 1
LENGTH: 8920
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Best Local Similarity
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TITLE OF INVENTION: Synthetase II
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
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EARLIER FILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER FILING DATE: 1993-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/150,741 CURRENT FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stewart et al.
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 3
                                                                                                                                                                                                                                                                       APPLICANT: GUTHMANN, Marcelo D.

APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
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                                                                                                                                                                                        CITY: Washington
                    APPLICATION NUMBER:
                                                                                                                                                           COUNTRY:
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                                                                                                                                                         UNITED STATES OF AMERICA
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JMBER: US/08/722,126A
08-ОСТ-1996
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Best Local Similarity
        APPLICATION NUMBER: PCT/US:
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109:
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROSET L.
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                     SOFTWARE: Patentin Rela
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,6
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FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
STATE: D.C.
REGISTRATION NUMBER:
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TOPOLOGY: li
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54..617
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                                                                                                                                                                                     Floppy disk
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                                                         IL 109257
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                                                                                                      PCT/US95/04258
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Pred. No. 4.8e-06;
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APPLICATION NUMBER: 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION UMBER: 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: P36,207
REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617),227,7400
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SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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                                                                                                                                                                           APPLICATION NUMBER: US/07/945,288
FILING DATE: 1920910
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS FROM TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thomas, Wayne R. APPLICANT: Chua, Kaw-Yan
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                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC
SOFTWARE: ASCII TEXT
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 4.8e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.7%;
Best Local Similarity 68.7%;
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                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/945,28

FILING DATE: 10 SEPTEMBER 1992

APPLICATION NUMBER: US 580,655

FILING DATE: 11 SEPTEMBER 1990

APPLICATION NUMBER: US 458,642

FILING DATE: 13 FEBRUARY 1990

ATTORNEY/AGENT INFORMATION:

NAME: MANDRAGOURAS, AMY E.

REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                               TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII TEXT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1019 AGACAATTTCTTATATGATTGTCACTAATTTATTTAAAATCAAAATTTTTAGAAAATGAA 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2030 atacacatttatttcttattttccctaattcattagactctcatattcttaaaaagaata 2089
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LENGTH: 1172 base pairs
                                                                                                                    REFERENCE/DOCKET NUMBER: IPOTELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
MOLECULE TYPE:
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STREET: UC
STREET: UC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1..738
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                             STRANDEDNESS: single
                                                TYPE: nucleic acid
                  TOPOLOGY:
                                                                    LENGTH: 1172 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 STATE STREET, SUITE 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                     US 07/945,288
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                                                                                                                                                                                      36,207
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                                                                                                                                                                          IPC-010CC (IMI-024)
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; LOCATION:
US-08-462-831-9
                                                                                   US-08-461-809-9
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APPLICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY,AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE,/DOCKET NUMBER: IPC-010CC (IMI-024)
   Matches
                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application Patent No. 5770202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 68.78; Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII TEXT CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                 FEATURE:
                                                                                                                                               MOLECULE TYPE:
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CITY: BOSTON
STATE: MA
                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                           STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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ZIP: 02109
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                                                                                                                                                                                                            LENGTH:
   79;
                  Similarity
                                                                                                                                                                                       nucleic acid
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60 STATE STREET, SUITE 510
   Conservative
                                                                                                                                                              linear
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              2.7%;
68.7%;
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              Score 57.4; DB 1; Pred. No. 2e-05;
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   Mismatches
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   36;
                             Length 1172;
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US-08-461-441-9
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                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 227-74
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,28
APPLICATION NUMBER: US 580,655
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
                                                            1019
2030 atacacatttatttcttattttccctaattcattagactctcatattcttaaaaaagaata 2089
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1172 base pairs
                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII TEXT CURRENT APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: 1
COUNTRY:
                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MANDRAGOURAS, AMY E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                          AGACAATTTCTTATATGATTGTCACTAATTTATTTAAAATCAAAATTTTTAGAAAATGAA 1078
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  linear
                                                                                                                                       2.7%;
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                                                                                                                                       Score 57.4; DB 1; Pred. No. 2e-05;
                                                                                                                       Mismatches
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                                                                                                                                                    Length 1172;
                                                                                                                       Indels
                                                                                                                       0;
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             Sequence 8, Application US/09092770
Patent No. 5973119
GENERAL INFORMATION:
APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins
FILE REFERENCE: A.524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application PC/TUS9308518 GENERAL INFORMATION:
APPLICANT:
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
CURRENT APPLICATION NUMBER: US/09/092,770
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: DERMATOPHAGO
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE 6 COCKFIELD
                                                                                                                                                                                                                                           1019 AGACAATTTCTTATATGATTGTCACTAATTTATTTAAAATCAAAATTTTTAGAAAATGAA 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,
APPLICATION NUMBER: US 07/945,
FILING DATE: 10 SEPTEMBER 1992
ATTORNEY/ACENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1172 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U. ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MANDRAGOURAS, AMY E. REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 79; Conserv
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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PATENTIN VET: 2.0
; SEQ ID NO 8
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Human
US-09-222-851-8
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; ORGANISM: Human
US-09-092-770-8
                                                                                                 Query Match 2.7%;
Best Local Similarity 30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09222851
Patent No. 6165753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 112; Conserv
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SEQ ID NO 8
LENGTH: 1215
                                                                                    Matches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/222,851
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: 09/092,770
EARLIER FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6165753el Cyclin E Genes and Proteins
FILE REFERENCE: A-524
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NUMBER OF SEQ ID NOS: 18
                       1233 atactggtctcatccctcgtctacgctccatcatggttcaatggattgtaaagcaatgtt 1292
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                                                                                  Conservative 68; Mismatches 180;
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                                                                                                 Score 57.4; DB 4;
Pred. No. 2e-05;
                                                                                                                       Length 1215;
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; NAME/KEY: misc_feature;
; LOCATION: (2961)..(3673);
; OTHER INFORMATION: n represents a, c,
US-09-342-681C-12
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                       US-09-111-730-5

; Sequence 5, Application US/09111730

; Patent No. 6274359
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                                                                                       RESULT 13
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GENERAL INFORMATION:
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Best Local Similarity 70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/342,681C CURRENT FILING DATE: 199-06-29 PRIOR APPLICATION NUMBER: 60/092,279 PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zonana et al. TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia FILE REFERENCE: 52978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/112,366 PRIOR FILING DATE: 1998-12-15 NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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; LOCATION: (24)..(1526)
US-09-111-730-5
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                                                Query Match
Best Local S
Matches 78
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EARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application US/09248335
Patent No. 6096504
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: O'GEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/248,335 CURRENT FILING DATE: 1999-02-10
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CURRENT FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 9
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APPLICANT: Hiromichi Suzuki
APPLICANT: Hiromichi Suzuki
TITLE OF INVENTION: 25-HYDROXYVITAMIN D3-1a-HYDROXYLASE AND DNA ENCODING THE HYDRO
FILE REFERENCE: 1074
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TYPE: DNA
                                                                                                                                                                   TYPE: DNA
                                                                                                                                                    ORGANISM: maize
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                                                Local Similarity hes 78; Conserv
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Conservative
                                                  Conservative
                                                                2.6%;
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                                                Score 56.4; DB 3;
Pred. No. 3.3e-05;
0; Mismatches 36;
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                                                  Indels
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APPLICANT: MCGONIGLE, BRIAN

APPLICANT: O'KREFE, DANIEL

TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES

FILE REFERENCE: CL-1108-A

CURRENT APPLICATION NUMBER: US/09/247,373B

CURRENT FILING DATE: 1999-02-10

PRIOR APPLICATION NUMBER: 08/924,747

PRIOR FILING DATE: 1997-09-05

NUMBER OF SEQ ID NOS: 56

SOFTWARE: Microsoft Office 97

SEQ ID NO 33

LENGTH: 1117

TYPE: DNA

PRIORALISM: SOYBEAN
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US-09-247-373B-33
; Sequence 33, Application US/09247373B
; Patent No. 6168954
Search completed: July 25, Job time: 11390 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE:
NAME/KEY: unsure
LOCATION: (1101)
OTHER INFORMATION: M-A OR C
NAME/KEY: unsure
LOCATION: (1104)
OTHER INFORMATION: M-A OR C
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (1116)
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2144
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SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1000.DAT:*

SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 1 2 1 3 C 4 C 5 6	Score 2144 1117.4 1123 78.4 63.4	Query Match 100.0 52.1 5.7 3.7 3.0 3.0	Ouery Ouery Match Length DB Match Length DB 100.0 2144 22 52.1 3970 22 5.7 3018 22 3.7 5204 24 3.0 545 22 3.0 1298 22		AAD21310 AAD21312 AAD21312 AAD21311 ABL32901 AAH70126 AAH72764	Description Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human immune Syste Human cervical can Human cervical can
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σι	63.4	3.0	1298	22	AAH72764	Human
7	63.4	3.0	6564	24	ABL32123	Human
œ	63.2	2.9	1672	22	AAF92066	Human PRO1063 cDNA
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31-MAR-2000; 2000US-193523P.

29-MAR-2001; 11-0CT-2001. WO200174144-A1

2001WO-US09875

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cDNA encoding for	Cervical	adult 1	Human metastasis a	Human immune syste	Chemically pretrea	Human immune syste	Human immune syste	Human breast cance	Human differential	Human colon cancer	Sequence encoding	Norwalk virus stra	Norwalk virus geno	Rat mast cell func	Mammalian mast cel	Carbamoy1-phosphat	Human immune syste	Human immune syste	Human immune syste	Human cDNA encodin	cancer		immune	Human cancer agent	3' nucleotide port	Human immune syste	Human breast cance	cDNA encoding for	Human colon cancer	Rat differential t	Human colorectal c	Human digestive sy	Human cervical can	Human PRO4063 (UNQ

ALIGNMENTS

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RESULT
AAD21310
Meiotic prophase I; chromosome 1; male sterile SDS mutant; apomixis; plant breeding; seed production; SDS protein; ss.
                                                                                                                                                                                                   AAD21310 standard; cDNA; 2144 BP
                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                           Arabidopsis thaliana SDS cDNA
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Best Local Similarity 100.0%;
Matches 2144; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses novel plant gene from Arabidopsis thaliana, designated SDS, which is associated with a failure to maintain homologue attachment during meiotic prophase I. The SDS gene is located on chromosome 1 and is useful in plant breeding to produce male sterile SDS mutants and cloned progeny by appointis where meiosis is bypassed in seed production. The gene may also be used as a probe to identify related genes in other plant species, and to identify and isolate other genes of the meiosis regulatory pathway. The present sequence is a cDNA encoding Arabidopsis thaliana SDS protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A new plant gene from Arabidopsis, designated SDS, mutations in which are associated with inability to produce pollen, is useful for the production of male sterile plants for plant breeding -
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1080	<pre>ctcgctctctgtacctccagttcaaggaacagttctgtagatccacgattcccaacga </pre>	NN	ДУ
1020 1020	ottoctotgattotoctatttoaca 	961 961	Qy Db
960	<pre>cgttcagagatatattcacagtattccgacttcgattactcggattacactccgtccat </pre>	901 901	Qy Db
900	toggaagaggtttoggattototogatgatgagtcatotgagca 	841 841	Db Qy
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Query Match

Local

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                                                  male sterile SDS mutants and cloned progeny by apomixis where meiosis is bypassed in seed production. The gene may also be used as a probe to identify related genes in other plant species, and to identify and isolate other genes of the meiosis regulatory pathway. The present sequence is SDS gene from Arabidopsis thalia
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3018
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                                                                                                                                             Conservative
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                                                                                                                                                                                                        BP; 996 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 1;
                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                  47pp; English.
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Pred. No. 9.1e-16;
                                                                                                                                                                                                        C; 476 G;
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                                                                                                                                                                                                                                          promoter DNA from
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, acy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes which are modified by the methylation of cytosines. The can be used in the diagnosis and treatment of immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 874; 32pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       including eye diseases such as retinopathy, neovascular glaucoma
caccatttgtgtcgctcatacacatttatttcttattttccctaattcattagactctca
                                                                                                                                                                                  agatttatatacctaatcgagctggacttaattagctcttagtataccaattattagtgc
                                                                                                                                                                                                                                                            166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention provides a number of human immune system are modified by the methylation of cytosines. The s
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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2000DE-1043826
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Pred. No. 1
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abnormal
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                                                                                                                                                                                                                      The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with
                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                          12-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cervical cancer;
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                      2038
                                                                                                                                             Sequence 545 BP; 200 A; 40 C;
                                                                                                                                                                            cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                        New
                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-DEC-1999;
                                                                                                                                                                    useful for gene therapy.
 220
                                                                                                                                                                                                                                                                                                       isolated nucleic acid for diagnosing and treating cervical cancer
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                                                                                                                                                                                                                                                                                            assessing and
                                                                                                                                                                                                                                                                      Page 319-320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                               2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
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99US-0171350.
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                                                                                                Score 63.4; DB 2
Pred. No. 0.00092
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                                                                                                                                             23 G;
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12-MAY-2000;
09-JUN-2000;
21-JUL-2000;
                                                                                                                                                                           The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful; to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
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                                                      2040 atttcttattttccctaattcattagactctcatattcttaaaaagaatatttccttgtt 2099
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21-DEC-1999;
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                                                                                                                                               Sequence 1298 BP;
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                                                                                                                                                                                                                                                                                                       isolated nucleic acid for diagnosing and treating cervical cancer
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                    l Similarity
79; Conserv
          assessing and detecting compounds
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2000US-0203791.
2000US-0210600.
2000US-0220114.
                                                                                       Conservative
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99US-0171350.
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                                                                                                                                               201 C;
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                                                                                                 Score 63.4; DB 2
Pred. No. 0.0011;
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                                                                                       Mismatches
                                                                                                                                               215 T;
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RESULT 7 ABL32123/c ID ABL321 XX

ABL32123

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                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzhelmer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis, and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                               1832 taagcaatcaaaaagaacaaaaaccctaaaaaccaggacacagtatactccgataccaaca 1891
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01-SEP-2000;
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199
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                                                     ccaccatttgtgtcgctcatacacatttatttcttattttccctaattcattagactctc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                       3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                                             ;0
                                                                                                                                                                                                                                                                                         Score 63.4; DB 2
Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                             Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:
                                                                                                                                                                                                                                                                                                      24;
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                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                    Length 6564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene, us
abnormal
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                          Gaps
                                                     140
 80
                                                                              2071
                                                                                                                                                                260
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2045 ttattttccctaattcattagactctcatattcttaaaaagaatatttccttgtttgaaa 2104

Matches

1 Similarity 77; Conserv

Conservative

0, Score Pred.

Mismatches 63.2; DB 2 No. 0.0012;

DB 22; 23;

Length

6

Indels

0;

Gaps

2.9%; 77.0%;

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RESULT AAF9UL66 ID FAF92066 ID FAF92066 ID FAF92066 ID FAF9206 ID FAF9206 ID FAF920 ID
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22-FEB-2000;
01-MAR-2000;
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15-SEP-1999;
07-DEC-1999;
09-DEC-1999;
11-JAN-2000;
18-FEB-2000;
                                                                                                                             The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular and the protein and the protein coding sequence has applications in molecular and the protein coding sequence has applications in molecular and the protein coding sequence has applications in molecular and the protein coding sequence has applications in molecular and the protein code in the protein coding sequence has applications in molecular and the protein code in the 
   Sequence 1672
                                                                                                       biology,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eighty four nucleic acids encoding I molecular biology, including use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grimaldi CJ,
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25-APR-2000;
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                                                                      mapping.
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                                                                                                   including use as hybridisation probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 17; 278pp;
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2000US-0187202.
2000US-0199397.
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2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
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2000US-0209832
   BP;
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   552 A; 281 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerritsen
Watanabe
   367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CK,
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s hybridization pro
   <u>ن</u>
   472 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful
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17-JUN-1998; 98US-0089538. 17-JUN-1998; 98US-0089598. 17-JUN-1998; 98US-0089599. 17-JUN-1998; 98US-0089600. 17-JUN-1998; 98US-0089653. 18-JUN-1998; 98US-0089801. 18-JUN-1998; 98US-0089801.											1999;	09-DEC-1999.	WO9963088-A2.	sapiens.	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.	Membrane-bound protein PRO1063 encoding cDNA.	-APR-2000 (first entry)	AAZ64982;	982 AAZ64982 standard; cDNA; 1701 BP.	0	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	ttttctttgctaatttggaagattaactcatttttaataaaattatgtctaagattaaaa 1602
PR PR PR PR	Р Р Р Р Р Р Р Р	פר קר קר קר	 ק ק ק ק ק	י קלק געק	קק קק קק	אַ אַק אָק	יי קל קל	ਸ਼ਵ ਸ਼ਵ	ਸ਼ੁਰੂ ਸ਼ੁਰੂ	PR PR PR	PR PR	אַק אַק	PR	קק אק	PR	PR PR	PR :	איז קק	ק קק קק	ק ק ק	PR PR	PR PR
17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 18-AUG-1998; 18-AUG-1998; 18-AUG-1998;	17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998;	11-AUG-1998; 11-AUG-1998; 12-AUG-1998; 17-AUG-1998;	04-AUG-1998; 10-AUG-1998; 10-AUG-1998; 10-AUG-1998;	04-AUG-1998; 04-AUG-1998; 04-AUG-1998; 04-AUG-1998;	20-JUL-1998; 30-JUL-1998; 04-AUG-1998;	നായതാ	ാനായയ	2-JUL-1998 2-JUL-1998 2-JUL-1998	1998		888	8 8 8	6 66 6	o a a	888	888	ဆိုထိ	2000	0000	200	661 661 661	
98US-0096891. 98US-0096894. 98US-0096897. 98US-0096949. 98US-0096949. 98US-0096950. 98US-0096959.	8US-0096766 8US-0096768 8US-0096773 8US-0096791 8US-0096867	8US-0096143 8US-0096146 8US-0096329 8US-0096757	8US-0095325 8US-0095916 8US-0095929 8US-0096012	8US-0095301 8US-0095302 8US-0095318	805-00 805-00 805-00	8US-00 8US-00 8US-00	805-00 805-00	808-00 808-00	00-508	8US-00	805-00 805-00	8US-00	8US-00	80S-00	BUS-00	8US-00	8US-00	8US-000	8US-00	8US-00	305-008	305-008

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                 Matches
Human; secreted and transmembrane protein; PRO; cytostatic;
                                                                                                                                                                                    sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents, Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1998;
18-AUG-1998;
19-AUG-1998;
                          Human PRO4063 (UNQ128) nucleotide sequence SEQ ID NO:114.
                                                     02-APR-2001
                                                                                                        AAF44128 standard; cDNA; 1701 BP
                                                                                                                                                                       1572 ttttctttgctaatttggaagattaactcatttttaataaaattatgtctaagattaaaa 1631
                                                                                                                                                                                                                                         2045 ttattttccctaattcattagactctcatattcttaaaaaggaatatttccttgtttgaaa 2104
                                                                                                                                                                                                                                                                                                                                                                                are useful as hybridization probes, in chromosome and gene mapping and the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE
                                                                                                                                                                                                                                                                                                                                               Sequence 1701 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-072883/06.
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24-AUG-1998;
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                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       recombinant techniques.
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Yuan J;
                                                                                                                                                                                                                                                                                Conservative
                                                   (first entry)
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98US-0097022.
98US-0097141.
98US-0097218.
98US-0097661.
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98US-0100634
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98US-0097986
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                                                                                                                                                                                                                                                                                                                                                 557
                                                                                                                                                                                                                                                                                           2.9%;
77.0%;
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3-0097955.
3-0097971.
                                                                                                                                                                                                                                                                                                                                              A; 288 C;
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                           Score 63.2; DB 21; Pred. No. 0.0012;
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                                                                                                                                                                                                                                                                                                                                              381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide
                                                                                                                                                                                                                                                                                                                                              475
                                                                                                                                                                                                                                                                                                                                              T; 0 other;
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                                                                                                                                                                                                                                                                                                      Length 1701;
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18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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20-DEC-1999;
05-JAN-2000;
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26-JUL-1999;
28-JUL-1999;
17-AUG-1999;
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23-JUN-1999;
07-JUL-1999;
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                                                                                                                                                                                                                                                      06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic assay; ss
                                                                                                                                                                                                                                                                                                                                                                                                              cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                                                                                                                                                                                                                                                      15-SEP-1999;
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2000WO-US06884.
2000WO-US07377.
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2000WO-US00376
2000WO-US03565
2000WO-US04341
2000WO-US04414
2000WO-US0404914
2000WO-US05004
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99US-0149396.
99WO-US21090.
99WO-US21547.
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99WO-US28313.
99WO-US28301.
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99WO-US30911
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Er Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams Eaton μ, r γ Godowski PJ; Paoni NF;

2001-032160/04. DB; AAB65177.

PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, specific cells, to cause targeted cell death antibodies, to

Claim 2 Fig 65; 935pp; English.

The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostantal activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65194 to AAB65300 represent human PRO polynucleotide and protein sequences. AAF44087 to AAF44269 and cancer sisolation of human PRO sequences.

Sequence 1701 BP; 557 A; 288 Ç 381 G; 475 T; 0 other;

Query Match Best Local Similarity 2.9%; Score Pred. 63.2; DB 22; No. 0.0012; Length 1701;

2118

appendicitis; chronic colit

colitis;

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RESULT 11
AAAH70080/c
ID AAH700
AC A
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                                                                                                                                                                                                                                                                         cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 313; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-2000;
09-JUN-2000;
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14-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                            cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the
                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel genes (AAH68727-AAH73383) associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated nucleic acid for diagnosing and treating cervical car
for assessing and detecting compounds for treating the cancer
                                                                                                                aagaactcctctacagatttatatacttaatcgagctggacttaattagctcttagtata 1998
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                   2001-375006/39.
                                                                                      AAAAANTTTTTTTNNANNTTTTTTTTTTCCCCCCTTTNNTAAAGAATTTTTTNTNAAA
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2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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26-JUL-2000;
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17-MAR-2000;
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2000US-0231244. 2000US-0231413. 2000US-0231414.

2000US-0230437. 2000US-0230438. 2000US-0231242. 2000US-0231243.

2000US-0232401. 2000US-0233063. 2000US-0233064.

2000US-0232398. 2000US-0232399. 2000US-0232400.

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06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive system antigen of the invention.
        Human colorectal cancer antigen cDNA SEQ ID NO:
                                  19-OCT-2001
                                                          AAI57565;
                                                                               AAI57565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - \frac{1}{2}
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DB; AAM92541.
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                                                                               standard;
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Colorectal cancer; colorectal cancer antigen; gene therapy; ss. plens. 2001: 2001WC-US01350. 2001: 2000WS-018658. 2000: 2000WS-018658. 2000: 2000WS-018659. 2000: 2000WS-018659. 2000: 2000WS-018664. 2000: 2000WS-018667. 2000: 2000WS-01867. 2000: 2000WS-018667. 2000: 2000WS-018759. 2000: 2000WS-018756. 2000WS-018756. 2000: 2000WS-018756. 2000WS-018756. 2000: 2000WS-018756. 2000: 2000WS-018756. 2000WS-018756. 2000: 2000WS-018756. 2000: 2000WS-018756.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     number of colorectal cancer antigens. These are shown in AAI57547-AAI57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer to the color and/or the color and/or the color and the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 216 BP; 103 A; 24 C; 26 G; 60 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO: 29; 522pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAM38587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME
WPI; 2001-483415/52
                                                                                                                                                                               31-JAN-2000; 2000DE-1004102.
                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                        WO200157058-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Differential transcription; human; rat; tumour cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat differential transcription-associated cDNA SEQ ID 630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH82121 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a colorectal cancer antigen coding sequence of
                                                 Grips M,
                                                                                                                                                                                                                                31-JAN-2001; 2001WO-EP01003
                                                                                                                           (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 aaaaaaaaaaaaaaaaaaaaaaaa 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 agtatagaacttataaaccaatatattgatatttttaaaacatttttacatataagtaaa 89
                                                                                                                                                                                                                                                                                                                                                                                                                                             modulator; Class II tumour suppressor gene; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-457727/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                                              Hellriegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                         Hinzmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.9%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCI INC
                                                                         В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255
                                                   Schmefer R, Z
Schmitz A, Sers

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; DB 22
Pred. No. 0.0015
                                                   Zuber J,
ers C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56;
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                                                                               Tchernitsa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and/or rectum
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AAH33177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              effects of an active compound (potential pharmaceutical) on a cell line, particularly for diagnosis and treatment of tumors, especially by modulating expression of (I) (by gene therapy, antisense RNA or ribozyme methods) or by modulating the amount and/or location of (I)-encoded polypeptides (by administration of the polypeptide or its activator, antibody (optionally as a conjugate) or inhibitor). The method allows identification of many Class II tumour suppressor genes (i.e. genes that are not primary targets for tumour-initiating mutations).

Ah881492-AAH82376 represent the human and rat derived nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between tumour and normal cells and which has cytostatic activity. (I) work as modulators of Ras activity by inducing expression of tumour suppressor genes. (I), and polypeptides encoded by them, are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2041 tttcttattttccctaattcattagactctcatattcttaaaaagaatatttccttgttt 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 255 BP; 74 A; 26 C; 43 G; 102 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 532-533; 579pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids differentially expressed between tumor and normal cells, useful for diagnosis or therapy of tumors and for screening active
                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH33177 standard; cDNA; 705 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a nucleic acid (I) with differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for diagnosis
             Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers \cdot
                                                           WPI; 2001-235357/24.
P-PSDB; AAG73746.
                                                                                                                                                                             29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                            05-APR-2001.
                                                                                                                                                                                                                                                                                           WO200122920-A2
                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           colorectal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer antigen encoding cDNA SEQ ID NO: 233.
                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                           Human; colon cancer; colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragments described in the method of the invention.
                                                                                                              Ruben SM,
                                                                                                                                                                                                                           28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITATITITIKTITIKGGCATTATAMCCTTTTTTTTTTTTTAAATITTCCCTTTTGG 99
                                                                                                              Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis or therapy and in screening to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                             99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.9%;
                                                                                                                                                                                                                                                                                                                                                           ss.
                                                                                                                Birse CE,
                                                                                                                                                                                                                                                                                                                                                                           cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon CC cancer-associated nucleic acid molecules (N) and proteins (P), where CC the proteins are collectively known as colon cancer antigens. The colon CC cancer antigens have cytostatic activity and can be used in gene CC diagnosis and treatment of diseases associated with inappropriate P CC expression. For example, N and P may be used in the prevention, CC associated with decreased expression by rectifying mutations or deletions CC in a patient's genome that affect the activity of P by expressing CC inactive proteins or to supplement the patients own production of P. CC Additionally, N may be used to produce the colon cancer-associated Ps, CC by inserting the nucleic acids into a host cell and culturing the cell conserting the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 CC and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 62; DB 22; Length 705; Best Local Similarity 62.5%; Pred. No. 0.0018; Matches 95; Conservative 1; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                2113 aaaaaaaaaaaaaaaaaaaaaaaaaa 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                         Sequence 705 BP; 258 A; 97 C; 99 G; 247 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2371; 9803pp; English.
                                                                                                          639 aaaaaaaaaaaaaaaaaaaaaaaaaaa 670
                                                                                                                                                                                               519 agtatagaacttataaaccaatatattgatatttttaaaacatttttacatataagtaaa 578
                                                                                                                                                                                                                                                                                                                                                                                0;
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